

RAW SEQUENCE LISTING PATENT APPLICATION US/08/716,169C

DATE: 03/25/98
TIME: 17:12:19

INPUT SET: S24411.raw

This Raw Listing contains the General
Information Section and up to the first 5

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: ANDERTON, STEPHEN MARK
5 VAN DER ZEE, RUURD
6 VAN EDEN, WILLEM
7 (ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS
8 PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE
9 TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES
10 (iii) NUMBER OF SEQUENCES: 6
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: THE WEBB LAW FIRM
13 (B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
14 (C) CITY: PITTSBURGH
15 (D) STATE: PENNSYLVANIA
16 (E) COUNTRY: UNITED STATES OF AMERICA
17 (F) ZIP: 15219-1818
18 (v) COMPUTER READABLE FORM:
19 (A) MEDIUM TYPE: 3.5" FLOPPY DISK
20 (B) COMPUTER: DIGITAL VENTURIS GL 6200
21 (C) OPERATING SYSTEM: DOS
22 (D) SOFTWARE: MICROSOFT WORD 2.0c
23 (vi) CURRENT APPLICATION DATA:
24 (A) APPLICATION NUMBER: 08/716,169
25 (B) FILING DATE: 18-SEP-1996
26 (C) CLASSIFICATION:
27 (vii) PRIOR APPLICATION DATA:
28 (A) APPLICATION NUMBER: PCT/NL95/00108
29 (B) FILING DATE: 21-MAR-1995
30 (2) INFORMATION FOR SEQ ID NO: 1:
31 (i) SEQUENCE CHARACTERISTICS:
32 (A) LENGTH: 540
33 (B) TYPE: AMINO ACID
34 (C) STRANDEDNESS: SINGLE
35 (D) TOPOLOGY: UNKNOWN
36 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
37 Met Ala Lys Thr Ile Ala Tyr Asp Glu Ala Arg Arg Gly Leu
38 1 5 10 15
39
40 Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu
41 20 25 30
42
43 Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala
44 35 40 45
45
46 Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu

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47		50		55		60
48						
49	Leu Glu Asp Pro Tyr	Glu Lys Ile Gly	Ala Glu Leu Val Lys	Glu		
50		65		70		75
51						
52	Val Ala Lys Lys Thr	Asp Asp Val Ala	Gly Asp Gly Thr Thr	Thr		
53		80		85		90
54						
55	Ala Thr Val Leu Ala	Gln Ala Leu Val	Arg Glu Gly Leu Arg	Asn		
56		95		100		105
57						
58	Val Ala Ala Gly	Ala Asn Pro Leu	Gly Val Lys Arg Gly	Ile Glu		
59		110		115		120
60						
61	Lys Ala Val Glu	Lys Val Thr Glu	Thr Leu Leu Lys Gly	Ala Lys		
62		125		130		135
63						
64	Glu Val Glu Thr	Lys Glu Gln Ile	Ala Ala Thr Ala	Ala Ile Ser		
65		140		145		150
66						
67	Ala Gly Asp Gln	Ser Ile Gly Asp	Leu Ile Ala Glu	Ala Met Asp		
68		155		160		165
69						
70	Lys Val Gly Asn	Glu Gly Val Ile	Thr Val Glu Glu	Ser Asn Thr		
71		170		175		180
72						
73	Phe Gly Leu Gln	Leu Glu Leu Thr	Glu Gly Met Arg	Phe Asp Lys		
74		185		190		195
75						
76	Gly Tyr Ile Ser	Gly Tyr Phe Val	Thr Asp Pro Glu	Arg Gln Glu		
77		200		205		210
78						
79	Ala Val Leu Glu	Asp Pro Tyr Ile	Leu Leu Val Ser	Ser Lys Val		
80		215		220		225
81						
82	Ser Thr Val Lys	Asp Leu Leu Pro	Leu Leu Glu	Lys Val Ile Gly		
83		230		235		240
84						
85	Ala Gly Lys Pro	Leu Leu Ile Ile	Ala Glu Asp Val	Glu Gly Glu		
86		245		250		255
87						
88	Ala Leu Ser Thr	Leu Val Val Asn	Lys Ile Arg Gly	Thr Phe Lys		
89		260		265		270
90						
91	Ser Val Ala Val	Lys Ala Pro Gly	Phe Gly Asp Arg	Arg Lys Ala		
92		275		280		285
93						
94	Met Leu Gln Asp	Met Ala Ile Leu	Thr Gly Gly Gln	Val Ile Ser		
95		290		295		300
96						
97	Glu Glu Val Gly	Leu Thr Leu Glu	Asn Ala Asp Leu	Ser Leu Leu		
98		305		310		315
99						

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100 Gly Lys Ala Arg Lys Val Val Val Thr Lys Asp Glu Thr Thr Ile
101           320           325           330
102
103 Val Glu Gly Ala Gly Asp Thr Asp Ala Ile Ala Gly Arg Val Ala
104           335           340           345
105
106 Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg
107           350           355           360
108
109 Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala
110           365           370           375
111
112 Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg
113           380           385           390
114
115 Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val
116           395           400           405
117
118 Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr Leu Leu Gln Ala
119           410           415           420
120
121 Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr
122           425           430           435
123
124 Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln
125           440           445           450
126
127 Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys
128           455           460           465
129
130 Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
131           470           475           480
132
133 Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys
134           485           490           495
135
136 Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu
137           500           505           510
138
139 Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu
140           515           520           525
141
142 Lys Ala Ser Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe
143           530           535           540
144
145 (2) INFORMATION FOR SEQ ID NO: 2:
146 (i) SEQUENCE CHARACTERISTICS:
147 (A) LENGTH: 333
148 (B) TYPE: AMINO ACID
149 (C) STRANDEDNESS: SINGLE
150 (D) TOPOLOGY: UNKNOWN
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
152 Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn

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153	1	5	10	15
154				
155	Val Phe Arg Ala	Ala Leu Lys Asn Pro	Asp Ile Glu Val Val	Ala
156		20	25	30
157				
158	Val Asn Asp Leu Thr	Asp Ala Asn Thr	Leu Ala His Leu Leu	Lys
159		35	40	45
160				
161	Tyr Asp Ser Val His	Gly Arg Leu Asp	Ala Glu Val Ser Val	Asn
162		50	55	60
163				
164	Gly Asn Asn Leu Val	Val Asn Gly Lys	Glu Ile Ile Val Lys	Ala
165		65	70	75
166				
167	Glu Arg Asp Pro Glu	Asn Leu Ala Trp	Gly Glu Ile Gly Val	Asp
168		80	85	90
169				
170	Ile Val Val Glu Ser	Thr Gly Arg Phe	Thr Lys Arg Glu Asp	Ala
171		95	100	105
172				
173	Ala Lys His Leu Glu	Ala Gly Ala Lys	Lys Val Ile Ile Ser	Ala
174		110	115	120
175				
176	Pro Ala Lys Asn Glu	Asp Ile Thr Ile	Val Met Gly Val Asn	Gln
177		125	130	135
178				
179	Asp Lys Tyr Asp Pro	Lys Ala His His	Val Ile Ser Asn Ala	Ser
180		140	145	150
181				
182	Cys Thr Thr Asn Cys	Leu Ala Pro Phe	Ala Lys Val Leu His	Glu
183		155	160	165
184				
185	Gln Phe Gly Ile Val	Arg Gly Met Met	Thr Thr Val His Ser	Tyr
186		170	175	180
187				
188	Thr Asn Asp Gln Arg	Ile Leu Asp Leu	Pro His Lys Asp Leu	Arg
189		185	190	195
190				
191	Arg Ala Arg Ala Ala	Ala Glu Ser Ile	Ile Pro Thr Thr Thr	Gly
192		200	205	210
193				
194	Ala Ala Lys Ala Val	Ala Leu Val Leu	Pro Glu Leu Lys Gly	Lys
195		215	220	225
196				
197	Leu Asn Gly Met Ala	Met Arg Val Pro	Thr Pro Asn Val Ser	Val
198		230	235	240
199				
200	Val Asp Leu Val Ala	Glu Leu Glu Lys	Glu Val Thr Val Glu	Glu
201		245	250	255
202				
203	Val Asn Ala Ala Leu	Lys Ala Ala Ala	Glu Gly Glu Leu Lys	Gly
204		260	265	270
205				

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206 Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn
207           275           280           285
208
209 Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val
210           290           295           300
211
212 Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu
213           305           310           315
214
215 Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala
216           320           325           330
217
218 Ser Lys Gly
219
220 (2) INFORMATION FOR SEQ ID NO: 3:
221 (i) SEQUENCE CHARACTERISTICS:
222 (A) LENGTH: 332
223 (B) TYPE: AMINO ACID
224 (C) STRANDEDNESS: SINGLE
225 (D) TOPOLOGY: UNKNOWN
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
227 Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
228 1           5           10           15
229
230 Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile
231           20           25           30
232
233 Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
234           35           40           45
235
236 Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu
237           50           55           60
238
239 Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln
240           65           70           75
241
242 Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu
243           80           85           90
244
245 Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala
246           95           100          105
247
248 Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala
249           110          115          120
250
251 Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu
252           125          130          135
253
254 Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr
255           140          145          150
256
257 Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe
258           155          160          165

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SEQUENCE VERIFICATION REPORT
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Original Text